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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,082

DATE: 03/21/2003

TIME: 13:45:24

Input Set : A:\P10890US.ST25.txt

Output Set: N:\CRF4\03212003\J069082.raw

3 <110> APPLICANT: Quip Technology Limited
 5 <120> TITLE OF INVENTION: Retrovirus Assay
 7 <130> FILE REFERENCE: P10890US
 9 <140> CURRENT APPLICATION NUMBER: US 10/069,082
 C--> 10 <141> CURRENT FILING DATE: 2002-10-30
 12 <150> PRIOR APPLICATION NUMBER: GB 9919604.0
 13 <151> PRIOR FILING DATE: 1999-08-18
 15 <150> PRIOR APPLICATION NUMBER: PCT/GB00/03159
 16 <151> PRIOR FILING DATE: 2000-08-16
 18 <160> NUMBER OF SEQ ID NOS: 19
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 524
 24 <212> TYPE: PRT
 25 <213> ORGANISM: porcine endogenous retrovirus
 27 <400> SEQUENCE: 1
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 30 1 5 10 15
 33 Thr Glu Val Arg Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys
 34 20 25 30
 37 Gly Pro Trp Gln Thr Phe Cys Ala Ser Glu Trp Pro Thr Phe Asp Val
 38 35 40 45
 41 Gly Trp Pro Ser Glu Gly Thr Phe Asn Ser Glu Ile Ile Leu Ala Val
 42 50 55 60
 45 Lys Ala Ile Ile Phe Gln Thr Gly Pro Gly Ser His Pro Asp Gln Glu
 46 65 70 75 80
 49 Pro Tyr Ile Leu Thr Trp Gln Asp Leu Ala Glu Asp Pro Pro Pro Trp
 50 85 90 95
 53 Val Lys Pro Trp Leu Asn Lys Pro Arg Lys Pro Gly Pro Arg Ile Leu
 54 100 105 110
 57 Ala Leu Gly Glu Lys Asn Lys His Ser Ala Glu Lys Val Glu Pro Ser
 58 115 120 125
 61 Ser Ser Tyr Leu Pro Arg Asp Arg Gly Ala Ala Asp Leu Ala Gly Thr
 62 130 135 140
 65 Pro Thr Cys Ser Pro Thr Pro Leu Ser Ser Thr Gly Cys Cys Glu Gly
 66 145 150 155 160
 69 Thr Ser Ala Pro Pro Gly Ala Pro Val Val Glu Gly Pro Ala Ala Gly
 70 165 170 175
 73 Thr Arg Ser Arg Arg Gly Ala Thr Pro Glu Arg Thr Asp Glu Ile Ala
 74 180 185 190
 77 Ile Leu Pro Leu Arg Thr Tyr Gly Pro Pro Met Pro Gly Gly Gln Leu
 78 195 200 205
 81 Gln Pro Leu Gln Tyr Trp Pro Phe Ser Ser Ala Asp Leu Tyr Asn Trp

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85 Lys Thr Asn His Pro Pro Phe Ser Glu Asp Pro Gln Arg Leu Thr Gly
86 225      230      235      240
89 Leu Val Glu Ser Leu Met Phe Ser His Gln Pro Thr Trp Asp Asp Cys
90      245      250      255
93 Gln Gln Leu Leu Gln Thr Leu Phe Thr Thr Glu Glu Arg Glu Arg Ile
94      260      265      270
97 Leu Leu Glu Ala Arg Lys Asn Val Pro Gly Ala Asp Gly Arg Pro Thr
98      275      280      285
101 Gln Leu Gln Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly
102      290      295      300
105 Trp Asp Tyr Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg
106 305      310      315      320
109 Gln Ala Leu Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn
110      325      330      335
113 Leu Ala Lys Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser
114      340      345      350
117 Val Phe Leu Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe
118      355      360      365
121 Asp Pro Thr Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile
122      370      375      380
125 Gly Gln Ser Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly
126 385      390      395      400
129 Leu Gln Glu Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val
130      405      410      415
133 Tyr Tyr Arg Arg Glu Thr Glu Glu Glu Lys Glu Gln Arg Lys Glu Lys
134      420      425      430
137 Glu Arg Glu Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn
138      435      440      445
141 Leu Thr Lys Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu
142      450      455      460
145 Arg Glu Arg Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly
146 465      470      475      480
149 Asn Leu Gly Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys
150      485      490      495
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162 <211> LENGTH: 660
163 <212> TYPE: PRT
164 <213> ORGANISM: porcine endogenous retrovirus Type PERV A
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169 1      5      10      15
172 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
173      20      25      30
176 Leu Thr Leu Ser Ile Thr Pro Gln Val Asn Gly Lys Arg Leu Val Asp

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180 Ser Pro Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp
181          50          55          60
184 Ser Gly Thr Gly Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu
185 65          70          75          80
188 Gly Thr Trp Trp Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
189          85          90          95
192 Gly Leu Asn Asp Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly
193          100          105          110
196 Phe Tyr Val Cys Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn
197          115          120          125
200 Pro Gln Asp Phe Phe Cys Lys Gln Trp Ser Cys Ile Thr Ser Asn Asp
201          130          135          140
204 Gly Asn Trp Lys Trp Pro Val Ser Gln Gln Asp Arg Val Ser Tyr Ser
205 145          150          155          160
208 Phe Val Asn Asn Pro Thr Ser Tyr Asn Gln Phe Asn Tyr Gly His Gly
209          165          170          175
212 Arg Trp Lys Asp Trp Gln Gln Arg Val Gln Lys Asp Val Arg Asn Lys
213          180          185          190
216 Gln Ile Ser Cys His Ser Leu Asp Leu Asp Tyr Leu Lys Ile Ser Phe
217          195          200          205
220 Thr Glu Lys Gly Lys Gln Glu Asn Ile Gln Lys Trp Val Asn Gly Ile
221          210          215          220
224 Ser Trp Gly Ile Val Tyr Tyr Gly Gly Ser Gly Arg Lys Lys Gly Ser
225 225          230          235          240
228 Val Leu Thr Ile Arg Leu Arg Ile Glu Thr Gln Met Glu Pro Pro Val
229          245          250          255
232 Ala Ile Gly Pro Asn Lys Gly Leu Ala Glu Gln Gly Pro Pro Ile Gln
233          260          265          270
236 Glu Gln Arg Pro Ser Pro Asn Pro Ser Asp Tyr Asn Thr Thr Ser Gly
237          275          280          285
240 Ser Val Pro Thr Glu Pro Asn Ile Thr Ile Lys Thr Gly Ala Lys Leu
241          290          295          300
244 Phe Ser Leu Ile Gln Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro
245 305          310          315          320
248 Glu Ala Thr Ser Ser Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr
249          325          330          335
252 Tyr Glu Gly Met Ala Arg Gly Gly Lys Phe Asn Val Thr Lys Glu His
253          340          345          350
256 Arg Asp Gln Cys Thr Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu
257          355          360          365
260 Val Ser Gly Lys Gly Thr Cys Ile Gly Met Val Pro Pro Ser His Gln
261          370          375          380
264 His Leu Cys Asn His Thr Glu Ala Phe Asn Arg Thr Ser Glu Ser Gln
265 385          390          395          400
268 Tyr Leu Val Pro Gly Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu
269          405          410          415
272 Thr Pro Cys Val Ser Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys
273          420          425          430

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276 Val Met Val Gln Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala
277      435      440      445
280 Val Leu Asp Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro
281      450      455      460
284 Ile Ser Leu Thr Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly
285 465      470      475      480
288 Val Gly Thr Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu
289      485      490      495
292 Lys Gly Leu Ser Asn Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala
293      500      505      510
296 Leu Glu Lys Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser
297      515      520      525
300 Glu Val Val Leu Gln Asn Arg Gly Leu Asp Leu Leu Phe Leu Lys
301      530      535      540
304 Glu Gly Gly Leu Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val
305 545      550      555      560
308 Asp His Ser Gly Ala Ile Arg Asp Ser Met Ser Lys Leu Arg Glu Arg
309      565      570      575
312 Leu Glu Arg Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu
313      580      585      590
316 Gly Trp Phe Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu
317      595      600      605
320 Thr Gly Pro Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys
321      610      615      620
324 Leu Ile Asn Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val
325 625      630      635      640
328 Gln Ile Met Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly
329      645      650      655
332 Glu Thr Asp Leu
333      660
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 638
338 <212> TYPE: PRT
339 <213> ORGANISM: porcine endogenous retrovirus Type PERV MSL
341 <400> SEQUENCE: 3
343 Met His Pro Thr Leu Asn Arg Arg His Leu Pro Ile Arg Gly Gly Lys
344 1      5      10      15
347 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
348      20      25      30
351 Leu Thr Leu Ser Ile Thr Ser Gln Thr Asn Gly Met Arg Ile Gly Asp
352      35      40      45
355 Ser Leu Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Ile Thr Asp
356      50      55      60
359 Ser Gly Thr Gly Ile Asn Ile Asn Asn Thr Gln Gly Glu Ala Pro Leu
360 65      70      75      80
363 Gly Thr Trp Trp Pro Asp Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
364      85      90      95
367 Ser Leu Thr Ser Pro Pro Asp Ile Leu His Ala His Gly Phe Tyr Val
368      100      105      110

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371 Cys Pro Gly Pro Pro Asn Asn Gly Lys His Cys Gly Asn Pro Arg Asp
372      115      120      125
375 Phe Phe Cys Lys Gln Trp Asn Cys Val Thr Ser Asn Asp Gly Tyr Trp
376      130      135      140
379 Lys Trp Pro Thr Ser Gln Gln Asp Arg Val Ser Phe Ser Tyr Val Asn
380 145      150      155      160
383 Thr Tyr Thr Ser Ser Gly Gln Phe Asn Tyr Leu Thr Trp Ile Arg Thr
384      165      170      175
387 Gly Ser Pro Lys Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser
388      180      185      190
391 Phe Thr Glu Lys Gly Lys Gln Glu Asn Ile Leu Lys Trp Val Asn Gly
392      195      200      205
395 Met Ser Trp Gly Met Val Tyr Tyr Gly Gly Ser Gly Lys Gln Pro Gly
396      210      215      220
399 Ser Ile Leu Thr Ile Arg Leu Lys Ile Asn Gln Leu Glu Pro Pro Met
400 225      230      235      240
403 Ala Ile Gly Pro Asn Thr Val Leu Thr Gly Gln Arg Pro Pro Thr Gln
404      245      250      255
407 Gly Pro Gly Pro Ser Ser Asn Ile Thr Ser Gly Ser Asp Pro Thr Glu
408      260      265      270
411 Ser Asn Ser Thr Thr Lys Met Gly Ala Lys Leu Phe Ser Leu Ile Gln
412      275      280      285
415 Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro Glu Ala Thr Ser Ser
416      290      295      300
419 Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr Tyr Glu Gly Met Ala
420 305      310      315      320
423 Arg Arg Gly Lys Phe Asn Val Thr Lys Glu His Arg Asp Gln Cys Thr
424      325      330      335
427 Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu Val Ser Gly Lys Gly
428      340      345      350
431 Thr Cys Ile Gly Lys Val Pro Pro Ser His Gln His Leu Cys Asn His
432      355      360      365
435 Thr Glu Ala Phe Asn Gln Thr Ser Glu Ser Gln Tyr Leu Val Pro Gly
436      370      375      380
439 Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Val Ser
440 385      390      395      400
443 Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys Ile Met Val Gln Ile
444      405      410      415
447 Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala Ile Leu Asp Glu Tyr
448      420      425      430
451 Asp Tyr Arg Asn His Arg Gln Lys Arg Glu Pro Ile Ser Leu Thr Leu
452      435      440      445
455 Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly Val Gly Thr Gly Thr
456      450      455      460
459 Ala Ala Leu Val Thr Gly Pro Gln Gln Leu Glu Thr Gly Leu Ser Asn
460 465      470      475      480
463 Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala Leu Glu Lys Ser Val
464      485      490      495
467 Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln

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VERIFICATION SUMMARY

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DATE: 03/21/2003

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date